SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (ii) TITLE OF THE INVENTION: CYCLIC-GMP PHOSPHODIESTERASE
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Dr.
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0442 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-855-0555
 - (B) TELEFAX: 650-845-4166
 - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 593 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: PROSNOT06
 - (B) CLONE: 828228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gly Ser Gly Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp
1 5 10 15

Ile Asp Gly Arg Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser 20 25 30

Ser Asp Ile Met Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn

40 45 Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp 55 60 Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro 75 70 Val Ala Ile Lys Gln Leu Ser Ala Gly Val Glu Asp Lys Arg Thr Thr 90 Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg Arg Val Val 100 105 Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser Gly Gln Val 120 125 Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu Gly Gln Arg 135 140 Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val 150 155 Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala Glu 165 170 Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu Gly 185 180 Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys Met 200 Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys Lys 215 220 Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp Val 230 235 Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala Leu 245 250 Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met Leu 260 265 270 Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp Phe 275 280 285 Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His Asp 290 295 Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys Val 310 315 320 Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu Lys 325 330 Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys His 345 340 Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala Arg 360 Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn His 375 380 His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn Ile 390 395 Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met 405 410 Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met 420 425 Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu 440 445 His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser 455 460 Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu 470 475 Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu 490 485 Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala 500 505 Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val 515 520 525 Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp 530 535 540 Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met

- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1997 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: PROSNOT06
 - (B) CLONE: 828228
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

				GTCCGAGTGC		60
CGCAGGATGG	GATCCGGCTC	CTCCAGCTAC	CGGCCCAAGG	CCATCTACCT	GGACATCGAT	120
GGACGCATTC	AGAAGGTAAT	CTTCAGCAAG	TACTGCAACT	CCAGCGACAT	CATGGACCTG	180
TTCTGCATCG	CCACCGGCCT	GCCTCGGAAC	ACGACCATCT	CCCTGCTGAC	CACCGACGAC	240
GCCATGGTCT	CCATCGACCC	CACCATGCCC	GCGAATTCAG	AACGCACTCC	GTACAAAGTG	300
AGACCTGTGG	CCATCAAGCA	ACTCTCCGCT	GGTGTCGAGG	ACAAGAGAAC	CACAAGCCGT	360
GGCCAGTCTG	CTGAGAGACC	ACTGAGGGAC	AGACGGGTTG	TGGGCCTGGA	GCAGCCCCGG	420
AGGGAAGGAG	CATTTGAAAG	TGGACAGGTA	GAGCCCAGGC	CCAGAGAGCC	CCAGGGCTGC	480
TACCAGGAAG	GCCAGCGCAT	CCCTCCAGAG	AGAGAAGAAT	TAATCCAGAG	CGTGCTGGCG	540
CAGGTTGCAG	AGCAGTTCTC	AAGAGCATTC	AAAATCAATG	AACTGAAAGC	TGAAGTTGCA	600
AATCACTTGG	CTGTCCTAGA	GAAACGCGTG	GAATTGGAAG	GACTAAAAGT	GGTGGAGATT	660
GAGAAATGCA	AGAGTGACAT	TAAGAAGATG	AGGGAGGAGC	TGGCGGCCAG	AAGCAGCAGG	720
ACCAACTGCC	CCTGTAAGTA	CAGTTTTTTG	GATAACCACA	AGAAGTTGAC	TCCTCGACGC	780
GATGTTCCCA	CTTACCCCAA	GTACCTGCTC	TCTCCAGAGA	CCATCGAGGC	CCTGCGGAAG	840
CCGACCTTTG	ACGTCTGGCT	TTGGGAGCCC	AATGAGATGC	TGAGCTGCCT	GGAGCACATG	900
TACCACGACC	TCGGGCTGGT	CAGGGACTTC	AGCATCAACC	CTGTCACCCT	CAGGAGGTGG	960
CTGTTCTGTG	TCCACGACAA	CTACAGAAAC	AACCCCTTCC	ACAACTTCCG	GCACTGCTTC	1020
TGCGTGGCCC	AGATGATGTA	CAGCATGGTC	TGGCTCTGCA	GTCTCCAGGA	GAAGTTCTCA	1080
CAAACGGATA	TCCTGATCCT	AATGACAGCG	GCCATCTGCC	ACGATCTGGA	CCATCCCGGC	1140
TACAACAACA	CGTACCAGAT	CAATGCCCGC	ACAGAGCTGG	CGGTCCGCTA	CAATGACATC	1200
TCACCGCTGG	AGAACCACCA	CTGCGCCGTG	GCCTTCCAGA	TCCTCGCCGA	GCCTGAGTGC	1260
AACATCTTCT	CCAACATCCC	ACCTGATGGG	TTCAAGCAGA	TCCGACAGGG	AATGATCACA	1320
TTAATCTTGG	CCACTGACAT	GGCAAGACAT	GCAGAAATTA	TGGATTCTTT	CAAAGAGAAA	1380
ATGGAGAATT	TTGACTACAG	CAACGAGGAG	CACATGACCC	TGCTGAAGAT	GATTTTGATA	1440
AAATGCTGTG	ATATCTCTAA	CGAGGTCCGT	CCAATGGAAG	TCGCAGAGCC	TTGGGTGGAC	1500
TGTTTATTAG	AGGAATATTT	TATGCAGAGC	GACCGTGAGA	AGTCAGAAGG	CCTTCCTGTG	1560
GCACCGTTCA	TGGACCGAGA	CAAAGTGACC	AAGGCCACAG	CCCAGATTGG	GTTCATCAAG	1620
TTTGTCCTGA	TCCCAATGTT	TGAAACAGTG	ACCAAGCTCT	TCCCCATGGT	TGAGGAGATC	1680
ATGCTGCAGC	CACTTTGGGA	ATCCCGAGAT	CGCTACGAGG	AGCTGAAGCG	GATAGATGAC	1740
GCCATGAAAG	AGTTACAGAA	GAAGACTGAC	AGCTTGACGT	CTGGGGCCAC	CGAGAAGTCC	1800
AGAGAGAGAA	GCAGAGATGT	GAAAAACAGT	GAAGGAGACT	GTGCCTGAGG	AAAGCGGGGG	1860
GCGTGGCTGC	AGTTCTGGAC	GGGCTGGCCG	AGCTGCGCGG	GATCCTTGTG	CAGGGAAGAG	1920
CTGCCCTGGG	CACCTGGCAC	CACAAGACCA	TGTTTTCTAA	GAACCATTTT	GTTCACTGAT	1980
ACAAAAAAAA	AAAAAA					1997

- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 713 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: THP1PLB02

(B) CLONE: 156196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Ala Cys Phe Leu Asp Lys His His Asp Ile Ile Ile Asp His Arg Asn Pro Arg Gln Leu Asp Ala Glu Ala Leu Cys Arg Ser Ile Arg 2.0 25 Ser Ser Lys Leu Ser Glu Asn Thr Val Ile Val Gly Val Val Arg Arg Val Asp Arg Glu Glu Leu Ser Val Met Pro Phe Ile Ser Ala Gly Phe 55 60 Thr Arg Arg Tyr Val Glu Asn Pro Asn Ile Met Ala Cys Tyr Asn Glu 75 Leu Leu Gln Leu Glu Phe Gly Glu Val Arg Ser Gln Leu Lys Leu Arg 85 90 Ala Cys Asn Ser Val Phe Thr Ala Leu Glu Asn Ser Glu Asp Ala Ile 105 Glu Ile Thr Ser Glu Asp Arg Phe Ile Gln Tyr Ala Asn Pro Ala Phe 115 120 125 Glu Thr Thr Met Gly Tyr Gln Ser Gly Glu Leu Ile Gly Lys Glu Leu 135 140 Gly Glu Val Pro Ile Asn Glu Lys Lys Ala Asp Leu Leu Asp Thr Ile 150 155 Asn Ser Cys Ile Arg Ile Gly Lys Glu Trp Gln Gly Ile Tyr Tyr Ala 165 170 Lys Lys Lys Asn Gly Asp Asn Ile Gln Gln Asn Val Lys Ile Ile Pro 180 185 190 Val Ile Gly Gln Gly Lys Ile Arg His Tyr Val Ser Ile Ile Arg 200 Val Cys Asn Gly Asn Asn Lys Ala Glu Lys Ile Ser Glu Cys Val Gln 215 220 Ser Asp Thr Arg Thr Asp Asn Gln Thr Gly Lys His Lys Asp Arg Arg 230 235 Lys Gly Ser Leu Asp Val Lys Ala Val Ala Ser Arg Ala Thr Glu Val 250 245 Ser Ser Gln Arg Arg His Ser Ser Met Ala Arg Ile His Ser Met Thr 260 265 Ile Glu Ala Pro Ile Thr Lys Val Ile Asn Val Ile Asn Ala Ala Gln 280 285 Glu Ser Ser Pro Met Pro Val Thr Glu Ala Leu Asp Arg Val Leu Glu 295 300 Ile Leu Arg Thr Thr Glu Leu Tyr Ser Pro Gln Phe Gly Ala Lys Asp 310 315 Asp Asp Pro His Ala Asn Asp Leu Val Gly Gly Leu Met Ser Asp Gly 325 330 Leu Arg Arg Leu Ser Gly Asn Glu Tyr Val Leu Ser Thr Lys Asn Thr 345 Gln Met Val Ser Ser Asn Ile Ile Thr Pro Ile Ser Leu Asp Asp Val 360 365 Pro Pro Arg Ile Ala Arg Ala Met Glu Asn Glu Glu Tyr Trp Asp Phe 375 Asp Ile Phe Glu Leu Glu Ala Ala Thr His Asn Arg Pro Leu Ile Tyr 390 395 Leu Gly Leu Lys Met Phe Ala Arg Phe Gly Ile Cys Glu Phe Leu His 410 Cys Ser Glu Ser Thr Leu Arg Ser Trp Leu Gln Ile Ile Glu Ala Asn 425 420 430 Tyr His Ser Ser Asn Pro Tyr His Asn Ser Thr His Ser Ala Asp Val 440 Leu His Ala Thr Ala Tyr Phe Leu Ser Lys Glu Arg Ile Lys Glu Thr 455 460 Leu Asp Pro Ile Asp Glu Val Ala Ala Leu Ile Ala Ala Thr Ile His 470 475 Asp Val Asp His Pro Gly Arg Thr Asn Ser Phe Leu Cys Asn Ala Gly 485 490

Ser Glu Leu Ala Ile Leu Tyr Asn Asp Thr Ala Val Leu Glu Ser His 500 505 His Ala Ala Leu Ala Phe Gln Leu Thr Thr Gly Asp Asp Lys Cys Asn 515 520 525 Ile Phe Lys Asn Met Glu Arg Asn Asp Tyr Arg Thr Leu Arg Gln Gly 535 540 Ile Ile Asp Met Val Leu Ala Thr Glu Met Thr Lys His Phe Glu His 555 550 Val Asn Lys Phe Val Asn Ser Ile Asn Lys Pro Leu Ala Thr Leu Glu 565 570 Glu Asn Gly Glu Thr Asp Lys Asn Gln Glu Val Ile Asn Thr Met Leu 580 585 590 Arg Thr Pro Glu Asn Arg Thr Leu Ile Lys Arg Met Leu Ile Lys Cys 595 600 Ala Asp Val Ser Asn Pro Cys Arg Pro Leu Gln Tyr Cys Ile Glu Trp 615 620 Ala Ala Arg Ile Ser Glu Glu Tyr Phe Ser Gln Thr Asp Glu Glu Lys 630 635 Gln Gln Gly Leu Pro Val Val Met Pro Val Phe Asp Arg Asn Thr Cys 645 650 655 Ser Ile Pro Lys Ser Gln Ile Ser Phe Ile Asp Tyr Phe Ile Thr Asp 665 Met Phe Asp Ala Trp Asp Ala Phe Val Asp Leu Pro Asp Leu Met Gln 675 680 685 His Leu Asp Asn Asn Phe Lys Tyr Trp Lys Gly Leu Asp Glu Met Lys 695 Leu Arg Asn Leu Arg Pro Pro Glu 710

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 584 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: GenBank
 - (B) CLONE: 829179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Phe Gln His Gln Thr Asn Pro Gly Gly Pro Thr Asn Arg Arg Arg 10 Pro Arg Asp Gln Glu Ile His Gln Glu Pro Arg Tyr Pro Lys Ala Arg 20 25 30 Arg His Thr Pro Ala Trp Pro Pro Thr Gln Ser Arg Ser Trp Thr Gly 40 45 Ala Ser Thr Ser Trp Arg Pro Ser Arg Pro Ile Ala Ala Ser Pro Thr 55 60 Trp Arg Arg Leu Ser Ser Asn Ala Cys Ser Thr Arg Ser Cys Arg Thr 70 75 Leu Ala Ser Pro Ala Asp Arg Glu Ile Arg Phe Pro Asn Ile Tyr Val 90 Pro His Phe Trp Asp Lys Gln Glu Phe Asp Leu Pro Ser Leu Arg 100 105 110 Val Glu Asp Asn Pro Glu Leu Val Ala Ala Asn Ala Ala Ala Gly Gln 120 125 Gln Ser Ala Gly Gln Tyr Ala Arg Ser Arg Ser Pro Arg Gly Pro Pro 135 140 Met Ser Gln Ile Ser Gly Val Lys Arg Pro Leu Ser His Thr Asn Ser 150 155 Phe Thr Gly Glu Arg Leu Pro Thr Phe Gly Val Glu Thr Pro Arg Glu 165 170 175 Asn Glu Leu Gly Thr Leu Leu Gly Glu Leu Asp Thr Trp Gly Ile Gln

180 185 Ile Phe Ser Ile Gly Glu Phe Ser Val Asn Arg Pro Leu Thr Cys Val 195 200 205 Ala Tyr Thr Ile Phe Gln Ser Arg Glu Leu Leu Thr Ser Leu Met Ile 215 220 Pro Pro Lys Thr Phe Leu Asn Phe Met Ser Thr Leu Glu Asp His Tyr 230 235 Val Lys Asp Asn Pro Phe His Asn Ser Leu His Ala Ala Asp Val Thr 245 250 Gln Ser Thr Asn Val Leu Leu Asn Thr Pro Ala Leu Glu Gly Val Phe 260 265 270 Thr Pro Leu Glu Val Gly Gly Ala Leu Phe Ala Ala Cys Ile His Asp 275 280 285 Val Asp His Pro Gly Leu Thr Asn Gln Phe Leu Val Asn Ser Ser Ser 295 300 Glu Leu Ala Leu Met Tyr Asn Asp Glu Ser Val Leu Glu Asn His His 310 315 Leu Ala Val Ala Phe Lys Leu Gln Asn Gln Gly Cys Asp Ile Phe 325 330 Cys Asn Met Gln Lys Lys Gln Arg Gln Thr Leu Arg Lys Met Val Ile 340 345 Asp Ile Val Leu Ser Thr Asp Met Ser Lys His Met Ser Leu Leu Ala 360 365 Asp Leu Lys Thr Met Val Glu Thr Lys Lys Val Ala Gly Ser Gly Val 375 380 Leu Leu Asp Asn Tyr Thr Asp Arg Ile Gln Val Leu Glu Asn Leu 390 395 Val His Cys Ala Asp Leu Ser Asn Pro Thr Lys Pro Leu Pro Leu Tyr 405 410 Lys Arg Trp Val Ala Leu Leu Met Glu Glu Phe Phe Leu Gln Gly Asp 420 425 Lys Glu Arg Glu Ser Gly Met Asp Ile Ser Pro Met Cys Asp Arg His 435 440 445 Asn Ala Thr Ile Glu Lys Ser Gln Val Gly Phe Ile Asp Tyr Ile Val 455 460 His Pro Leu Trp Glu Thr Trp Ala Ser Leu Val His Pro Asp Ala Gln 470 475 Asp Ile Leu Asp Thr Leu Glu Glu Asn Arg Asp Tyr Tyr Gln Ser Met 490 Ile Pro Pro Ser Pro Pro Pro Ser Gly Val Asp Glu Asn Pro Gln Glu 500 505 Asp Arg Ile Arg Phe Gln Val Thr Leu Glu Glu Ser Asp Gln Glu Asn 520 525 Leu Ala Glu Leu Glu Glu Gly Asp Glu Ser Gly Gly Glu Thr Thr 530 535 540 Thr Gly Thr Thr Gly Thr Thr Ala Ala Ser Ala Leu Arg Ala Gly Gly 550 555 Gly Gly Gly Gly Gly Met Ala Pro Arg Thr Gly Gly Cys Gln 565 570 Asn Gln Pro Gln His Gly Gly Met

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGTGACAGG GTTGATGCT

(2) INFORMATION FOR SEQ ID NO:6:

19

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:			
TCGCTTAGTT TTACCGTTTT C			
(2) INFORMATION FOR SEQ ID NO:7:			
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 22 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:			
TATCGCCTCC ATCAACAAAC TT	22		
(2) INFORMATION FOR SEQ ID NO:8:			
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 19 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:			
GACACAGAAC AGCCACCTC	19		
(2) INFORMATION FOR SEQ ID NO:9:			
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:			
AGCAAGTTCA GCCTGGTTAA G	21		
(2) INFORMATION FOR SEQ ID NO:10:			
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 24 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:			
CTTATGAGTA TTTCTTCCAG GGTA			
(2) INFORMATION FOR SEQ ID NO:11:			
(i) SEQUENCE CHARACTERISTICS:			

(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:			
ATCATGGTTA CAAATTATCG AAGCCAATTA	30		
(2) INFORMATION FOR SEQ ID NO:12:			
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:			
GCTCCTCCT CATCTTCTTA	20		
(2) INFORMATION FOR SEQ ID NO:13:			
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:			
AGGACAGCCA AGTGATTT			
(2) INFORMATION FOR SEQ ID NO:14:			
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:			
TGCGCTGGCC TTCCTGGTAG	20		